

GFAT-anglais

SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> GLUTAMINE:FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (GFAT) COMPRISING AN INTERNAL PURIFICATION TAG, AND ITS USE FOR THE SCREENING OF COMPOUNDS

<130> WOB 03 BP CNR GFAT

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 2046

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2046)

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cga	gaa	atc	ctg	gag	acc	cta	atc	aaa	ggc	ctt	cag	aga	ctg	gag	tac	96
Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
			20					25					30			

aga	gga	tat	gat	tct	gct	ggt	gtg	gga	ttt	gat	gga	ggc	aat	gat	aaa	144
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys	
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gat	tgg	gaa	gcc	aat	gcc	tgc	aaa	anc	cag	ctt	att	aag	aag	aaa	gga	192
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly	
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aaa	ggt	aag	gca	ctg	gat	gaa	gaa	ggt	cac	aag	caa	caa	gat	atg	gat	240
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp	
65					70				75					80		

ttg	gat	ata	gaa	ttt	gat	gta	cac	ctt	gga	ata	gct	cat	acc	cgt	tgg	288
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp	
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gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct	336
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	
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gat	aaa	aat	aat	gaa	ttt	atc	ggt	att	cac	aat	gga	atc	atc	acc	aac	384
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GFAT-anglais															
Asp	Lys	Asn 115	Asn	Glu	Phe	Ile	Val 120	Ile	His	Asn	Gly	Ile 125	Ile	Thr	Asn
tac Tyr	aaa Lys 130	gac Asp	ttg Leu	aaa Lys	aag Lys	ttt Phe 135	ttg Leu	gaa Glu	agc Ser	aaa Lys	ggc Gly 140	tat Tyr	gac Asp	ttc Phe	gaa Glu
tct Ser 145	gaa Glu	aca Thr	gac Asp	aca Thr	gag Glu 150	aca Thr	att Ile	gcc Ala	aag Lys	ctc Leu 155	ggt Val	aag Lys	tat Tyr	atg Met	tat Tyr 160
gac Asp	aat Asn	cgg Arg	gaa Glu	agt Ser 165	caa Gln	gat Asp	acc Thr	agc Ser	ttt Phe 170	act Thr	acc Thr	ttg Leu	gtg Val	gag Glu 175	aga Arg
ggt Val	atc Ile	caa Gln 180	caa Gln	ttg Leu	gaa Glu	ggt Gly	gct Ala	ttt Phe 185	gca Ala	ctt Leu	gtg Val	ttt Phe 190	aaa Lys	agt Ser	gtt Val
cat His	ttt Phe	ccc Pro 195	ggg Gly	caa Gln	gca Ala	gtt Val	ggc Gly 200	aca Thr	agg Arg	cga Arg	ggt Gly	agc Ser 205	cct Pro	ctg Leu	ttg Leu
att Ile	ggt Gly 210	gta Val	cgg Arg	agt Ser	gaa Glu	cat His 215	aaa Lys	ctt Leu	tct Ser	act Thr	gat Asp 220	cac His	att Ile	cct Pro	ata Ile
ctc Leu 225	tac Tyr	aga Arg	aca Thr	ggc Gly	aaa Lys 230	gac Asp	aag Lys	aaa Lys	gga Gly	agc Ser 235	tgc Cys	aat Asn	ctc Leu	tct Ser	cgt Arg 240
gtg Val	gac Asp	agc Ser	aca Thr	acc Thr 245	tgc Cys	ctt Leu	ttc Phe	ccg Pro	gtg Val 250	gaa Glu	gaa Glu	aaa Lys	gca Ala	gtg Val 255	gag Glu
tat Tyr	tac Tyr	ttt Phe 260	gct Ala	tct Ser	gat Asp	gca Ala	agt Ser	gct Ala 265	gtc Val	ata Ile	gaa Glu	cac His	acc Thr 270	aat Asn	cgc Arg
gtc Val	atc Ile	ttt Phe 275	ctg Leu	gaa Glu	gat Asp	gat Asp 280	gat Asp	gtt Val	gca Ala	gca Ala	gta Val	gtg Val 285	gat Asp	gga Gly	cgt Arg
ctt Leu 290	tct Ser	atc Ile	cat His	cga Arg	att Ile	aaa Lys 295	cga Arg	act Thr	gca Ala	gga Gly	gat Asp 300	cac His	ccc Pro	gga Gly	cga Arg
gct Ala 305	gtg Val	caa Gln	aca Thr	ctc Leu	cag Gln 310	atg Met	gaa Glu	ctc Leu	cag Gln	cag Gln 315	atc Ile	atg Met	aag Lys	ggc Gly	aac Asn 320
ttc Phe	agt Ser	tca Ser	ttt Phe	atg Met 325	cag Gln	aag Lys	gaa Glu	ata Ile	ttt Phe 330	gag Glu	cag Gln	cca Pro	gag Glu	tct Ser 335	gtc Val
gtg Val	aac Asn	aca Thr	atg Met 340	aga Arg	gga Gly	aga Arg	gtc Val	aac Asn 345	ttt Phe	gat Asp	gac Asp	tat Tyr	act Thr 350	gtg Val	aat Asn
ttg Leu	ggt Gly	ggt Gly	ttg Leu	aag Lys	gat Asp	cac His	ata Ile	aag Lys	gag Glu	atc Ile	cag Gln	aga Arg	tgc Cys	cgg Arg	cgt Arg

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ttg	att	ctt	att	gct	tgt	gga	aca	agt	tac	cat	gct	ggt	gta	gca	aca			1152
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cgt	caa	ggt	ctt	gag	gag	ctg	act	gag	ttg	cct	gtg	atg	gtg	gaa	cta			1200
Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	Pro	Val	Met	Val	Glu	Leu			
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gca	agt	gac	ttc	ctg	gac	aga	aac	aca	cca	gtc	ttt	cga	gat	gat	ggt			1248
Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	Val	Phe	Arg	Asp	Asp	Val			
				405					410					415				
tgc	ttt	ttc	ctt	agt	caa	tca	ggt	gag	aca	gca	gat	act	ttg	atg	ggt			1296
Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly			
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ctt	cgt	tac	tgt	aag	gag	aga	gga	gct	tta	act	gtg	ggg	atc	aca	aac			1344
Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn			
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aca	ggt	ggc	agt	tcc	ata	tca	cgg	gag	aca	gat	tgt	gga	ggt	cat	att			1392
Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val	His	Ile			
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aat	gct	ggt	cct	gag	att	ggt	gtg	gcc	agt	aca	aag	gct	tat	acc	agc			1440
Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser			
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Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu	Met	Met	Cys	Asp	Asp	Arg			
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atc	tcc	atg	caa	gaa	aga	cgc	aaa	gag	atc	atg	ctt	gga	ttg	aaa	cgg			1536
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ctg	cct	gat	ttg	att	aag	gaa	gta	ctg	agc	atg	gat	gac	gaa	att	cag			1584
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aaa	cta	gca	aca	gaa	ctt	tat	cat	cag	aag	tca	ggt	ctg	ata	atg	gga			1632
Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys	Ser	Val	Leu	Ile	Met	Gly			
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cga	ggc	tat	cat	tat	gct	act	tgt	ctt	gaa	ggg	gca	ctg	aaa	atc	aaa			1680
Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys			
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Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu	Leu	Lys			
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cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg	atg	cct	gtg	atc	atg	atc			1776
His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	Met	Pro	Val	Ile	Met	Ile			
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Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	Gln	Asn	Ala	Leu	Gln	Gln			
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gtg	gtt	gct	cgg	cag	ggg	cgg	cct	gtg	gta	att	tgt	gat	aag	gag	gat	1872
Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	Ile	Cys	Asp	Lys	Glu	Asp	
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act	gag	acc	att	aag	aac	aca	aaa	aga	acg	atc	aag	gtg	ccc	cac	tca	1920
Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	Ile	Lys	Val	Pro	His	Ser	
625					630					635					640	
gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	atc	cct	tta	cag	ttg	ctg	1968
Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	Ile	Pro	Leu	Gln	Leu	Leu	
				645					650					655		
gct	ttc	cac	ctt	gct	gtg	ctg	aga	ggc	tat	gat	gtt	gat	ttc	cca	cgg	2016
Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	Asp	Val	Asp	Phe	Pro	Arg	
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 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
 115 120 125
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
 130 135 140
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
 145 150 155 160

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Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
 165 170 175
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
 180 185 190
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
 195 200 205
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
 210 215 220
 Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg
 225 230 235 240
 Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu
 245 250 255
 Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg
 260 265 270
 Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg
 275 280 285
 Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro Gly Arg
 290 295 300
 Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly Asn
 305 310 315 320
 Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser Val
 325 330 335
 Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr Val Asn
 340 345 350
 Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys Arg Arg
 355 360 365
 Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val Ala Thr
 370 375 380
 Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu Leu
 385 390 395 400
 Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp Val
 405 410 415
 Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Met Gly
 420 425 430
 Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile Thr Asn
 435 440 445
 Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His Ile
 450 455 460
 Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser
 465 470 475 480
 Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp Asp Arg

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490

485

495

Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu Lys Arg
500 505 510
Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu Ile Gln
515 520 525
Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile Met Gly
530 535 540
Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile Lys
545 550 555 560
Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu Lys
565 570 575
His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile Met Ile
580 585 590
Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu Gln Gln
595 600 605
Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys Glu Asp
610 615 620
Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro His Ser
625 630 635 640
Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu Leu
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Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
20 25 30
aga ggc tac gac tcg gca ggt gtg gcg atc gat ggg aat aat cac gaa 144
Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu
35 40 45
gtc aaa gaa aga cac att cag ctg gtc aag aaa agg ggg aaa gtc aag 192

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Ala	Leu	Asp	Glu	Glu	Leu	Tyr	Lys	Gln	Asp	Ser	Met	Asp	Leu	Lys	Val
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gag	ttt	gag	aca	cac	ttc	ggc	att	gcc	cac	acg	cgc	tgg	gcc	acc	cac
Glu	Phe	Glu	Thr	His	Phe	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His
				85					90					95	
ggg	gtc	ccc	agt	gct	gtc	aac	agc	cac	cct	cag	cgc	tca	gac	aaa	ggc
Gly	Val	Pro	Ser	Ala	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	Asp	Lys	Gly
			100					105					110		
aac	gaa	ttt	gtt	gtc	atc	cac	aat	ggg	atc	atc	aca	aat	tac	aaa	gat
Asn	Glu	Phe	Val	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	Tyr	Lys	Asp
		115					120					125			
ctg	agg	aaa	ttt	ctg	gaa	agc	aaa	ggc	tac	gag	ttt	gag	tca	gaa	aca
Leu	Arg	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Glu	Phe	Glu	Ser	Glu	Thr
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Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Ile	Lys	Tyr	Val	Phe	Asp	Asn	Arg
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gaa	act	gag	gac	att	acg	ttt	tca	acg	ttg	gtc	gag	aga	gtc	att	cag
Glu	Thr	Glu	Asp	Ile	Thr	Phe	Ser	Thr	Leu	Val	Glu	Arg	Val	Ile	Gln
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Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	His	Tyr	Pro
			180					185					190		
gga	gaa	gcc	gtt	gcc	aca	cgg	aga	ggc	agc	ccc	ctg	ctc	atc	gga	gtc
Gly	Glu	Ala	Val	Ala	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	Ile	Gly	Val
		195					200					205			
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Arg	Ser	Lys	Tyr	Lys	Leu	Ser	Thr	Glu	Gln	Ile	Pro	Ile	Leu	Tyr	Arg
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Thr	Cys	Thr	Leu	Glu	Asn	Val	Lys	Asn	Ile	Cys	Lys	Thr	Arg	Met	Lys
225					230					235					240
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Arg	Leu	Asp	Ser	Ser	Ala	Cys	Leu	His	Ala	Val	Gly	Asp	Lys	Ala	Val
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gaa	ttc	ttc	ttt	gct	tct	gat	gca	agc	gct	atc	ata	gag	cac	acc	aac
Glu	Phe	Phe	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Ile	Ile	Glu	His	Thr	Asn
			260					265					270		
cgg	gtc	atc	ttc	ctg	gag	gac	gat	gac	atc	gcc	gca	gtg	gct	gat	ggg
Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Ile	Ala	Ala	Val	Ala	Asp	Gly
		275					280					285			
aaa	ctc	tcc	att	cac	cgg	gtc	aag	cgc	tcg	gcc	agt	gat	gac	cca	tct
Lys	Leu	Ser	Ile	His	Arg	Val	Lys	Arg	Ser	Ala	Ser	Asp	Asp	Pro	Ser

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300

290	295																
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aac Asn	ttc Phe	agt Ser	gcg Ala	ttt Phe 325	atg Met	cag Gln	aag Lys	gag Glu	atc Ile 330	ttc Phe	gaa Glu	cag Gln	cca Pro	gaa Glu 335	tca Ser		1008
gtt Val	ttc Phe	aat Asn	act Thr 340	atg Met	aga Arg	ggt Gly	cgg Arg	gtg Val 345	aat Asn	ttt Phe	gaa Glu	acc Thr	aac Asn 350	aca Thr	gtg Val		1056
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cgg Arg 370	ctc Leu	atc Ile	gtg Val	att Ile	ggc Gly	tgt Cys 375	gga Gly	acc Thr	agc Ser	tac Tyr	cac His 380	gct Ala	gcc Ala	gtg Val	gct Ala		1152
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ctt Leu	gct Ala	agt Ser	gat Asp	ttt Phe 405	ctg Leu	gac Asp	agg Arg	aac Asn	aca Thr 410	cct Pro	gtg Val	ttc Phe	agg Arg	gat Asp 415	gac Asp		1248
gtt Val	tgc Cys	ttt Phe	ttc Phe 420	atc Ile	agc Ser	cag Gln	tca Ser	ggc Gly 425	gag Glu	acc Thr	gcg Ala	gac Asp	acc Thr 430	ctc Leu	ctg Leu		1296
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atc Ile 465	aac Asn	gca Ala	ggg Gly	ccg Pro	gag Glu 470	gtc Val	ggc Gly	gtg Val	gcc Ala	agc Ser 475	acc Thr	aag Lys	gct Ala	tat Tyr	acc Thr 480		1440
agt Ser	cag Gln	ttc Phe	atc Ile	tct Ser 485	ctg Leu	gtg Val	atg Met	ttt Phe	ggt Gly 490	ttg Leu	atg Met	atg Met	tct Ser	gaa Glu 495	gac Asp		1488
cga Arg	att Ile	tca Ser	cta Leu 500	caa Gln	aac Asn	agg Arg	agg Arg	caa Gln 505	gag Glu	atc Ile	atc Ile	cgt Arg	ggc Gly 510	ttg Leu	aga Arg		1536
tct Ser	tta Leu	cct Pro 515	gag Glu	ctg Leu	atc Ile	aag Lys	gaa Glu 520	gtg Val	ctg Leu	tct Ser	ctg Leu	gag Glu 525	gag Glu	aag Lys	atc Ile		1584
cac His 530	gac Asp	ttg Leu	gcc Ala	ctg Leu	gag Glu	ctc Leu 535	tac Tyr	acg Thr	cag Gln	aga Arg	tgc Ser 540	ctg Leu	ctg Leu	gtg Val	atg Met		1632

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ggg Gly 545	cgg Arg	ggc Gly	tac Tyr	aac Asn	tat Tyr 550	gcc Ala	acc Thr	tgc Cys	ctg Leu	gaa Glu 555	gga Gly	gcc Ala	ctg Leu	aaa Lys	att Ile 560	1680
aaa Lys	gag Glu	ata Ile	acc Thr	tac Tyr 565	atg Met	cac His	tca Ser	gaa Glu	ggc Gly 570	atc Ile	ctg Leu	gct Ala	ggg Gly	gag Glu 575	ctg Leu	1728
aag Lys	cac His	ggg Gly	ccc Pro 580	ctg Leu	gca Ala	ctg Leu	att Ile	gac Asp 585	aag Lys	cag Gln	atg Met	ccc Pro	gtc Val 590	atc Ile	atg Met	1776
gtc Val	att Ile	atg Met 595	aag Lys	gat Asp	cct Pro	tgc Cys	ttc Phe 600	gcc Ala	aaa Lys	tgc Cys	cag Gln	aac Asn 605	gcc Ala	ctg Leu	cag Gln	1824
caa Gln 610	gtc Val	acg Thr	gcc Ala	cgc Arg	cag Gln	ggg Gly 615	cgc Arg	ccc Pro	att Ile	ata Ile	ctg Leu 620	tgc Cys	tcc Ser	aag Lys	gac Asp	1872
gat Asp 625	act Thr	gaa Glu	agt Ser	tcc Ser	aag Lys 630	ttt Phe	gcg Ala	tat Tyr	aag Lys	aca Thr 635	atc Ile	gag Glu	ctg Leu	ccc Pro	cac His 640	1920
act Thr	gtg Val	gac Asp	tgc Cys	ctc Leu 645	cag Gln	ggc Gly	atc Ile	ctg Leu	agc Ser 650	gtg Val	att Ile	ccg Pro	ctg Leu	cag Gln 655	ctg Leu	1968
ctg Leu	tcc Ser	ttc Phe	cac His 660	ctg Leu	gct Ala	gtt Val	ctc Leu	cga Arg 665	gga Gly	tat Tyr	gac Asp	gtt Val	gac Asp 670	ttc Phe	ccc Pro	2016
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys
 50 55 60
 Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val
 65 70 75 80
 Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His
 85 90 95

Gly Val Pro Ser Ala Val Asn Ser His GFAT-anglais
 100 105 Pro Gln Arg Ser Asp Lys Gly
 Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp
 115 120 125
 Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr
 130 135 140
 Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg
 145 150 155 160
 Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln
 165 170 175
 Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro
 180 185 190
 Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val
 195 200 205
 Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg
 210 215 220
 Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys
 225 230 235 240
 Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val
 245 250 255
 Glu Phe Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn
 260 265 270
 Arg Val Ile Phe Leu Glu Asp Asp Asp Ile Ala Ala Val Ala Asp Gly
 275 280 285
 Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser Asp Asp Pro Ser
 290 295 300
 Arg Ala Ile Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly
 305 310 315 320
 Asn Phe Ser Ala Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser
 325 330 335
 Val Phe Asn Thr Met Arg Gly Arg Val Asn Phe Glu Thr Asn Thr Val
 340 345 350
 Leu Leu Gly Gly Leu Lys Asp His Leu Lys Glu Ile Arg Arg Cys Arg
 355 360 365
 Arg Leu Ile Val Ile Gly Cys Gly Thr Ser Tyr His Ala Ala Val Ala
 370 375 380
 Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu
 385 390 395 400
 Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp
 405 410 415
 Val Cys Phe Phe Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Leu
 420 425 430

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Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala Leu Thr Val Gly Val Thr
435 440 445
Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His
450 455 460
Ile Asn Ala Gly Pro Glu Val Gly Val Ala Ser Thr Lys Ala Tyr Thr
465 470 475 480
Ser Gln Phe Ile Ser Leu Val Met Phe Gly Leu Met Met Ser Glu Asp
485 490 495
Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu Ile Ile Arg Gly Leu Arg
500 505 510
Ser Leu Pro Glu Leu Ile Lys Glu Val Leu Ser Leu Glu Glu Lys Ile
515 520 525
His Asp Leu Ala Leu Glu Leu Tyr Thr Gln Arg Ser Leu Leu Val Met
530 535 540
Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile
545 550 555 560
Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu
565 570 575
Lys His Gly Pro Leu Ala Leu Ile Asp Lys Gln Met Pro Val Ile Met
580 585 590
Val Ile Met Lys Asp Pro Cys Phe Ala Lys Cys Gln Asn Ala Leu Gln
595 600 605
Gln Val Thr Ala Arg Gln Gly Arg Pro Ile Ile Leu Cys Ser Lys Asp
610 615 620
Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys Thr Ile Glu Leu Pro His
625 630 635 640
Thr Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu
645 650 655
Leu Ser Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe Pro
660 665 670
Arg Asn Leu Ala Lys Ser Val Thr Val Glu
675 680

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<211> 2100
<212> DNA
<213> Homo sapiens

<220>
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<223>

GFAT-anglais

<220>
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 <222> (170)..(170)
 <223> t or c

<400> 5

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Met	Cys	Gly	Ile	Phe	Ala	Tyr	Leu	Asn	Tyr	His	Val	Pro	Arg	Thr	Arg	
1				5					10					15		
cga	gaa	atc	ctg	gag	acc	cta	atc	aaa	ggc	ctt	cag	aga	ctg	gag	tac	96
Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
			20					25					30			
aga	gga	tat	gat	tct	gct	ggt	gtg	gga	ttt	gat	gga	ggc	aat	gat	aaa	144
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys	
		35					40					45				
gat	tgg	gaa	gcc	aat	gcc	tgc	aaa	anc	cag	ctt	att	aag	aag	aaa	gga	192
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly	
	50					55					60					
aaa	ggt	aag	gca	ctg	gat	gaa	gaa	ggt	cac	aag	caa	caa	gat	atg	gat	240
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp	
65					70					75					80	
ttg	gat	ata	gaa	ttt	gat	gta	cac	ctt	gga	ata	gct	cat	acc	cgt	tgg	288
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp	
				85					90					95		
gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct	336
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	
			100					105					110			
gat	aaa	aat	aat	gaa	ttt	atc	ggt	att	cac	aat	gga	atc	atc	acc	aac	384
Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	
		115					120					125				
tac	aaa	gac	ttg	aaa	aag	ttt	ttg	gaa	agc	aaa	ggc	tat	gac	ttc	gaa	432
Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu	
	130					135					140					
tct	gaa	aca	gac	aca	gag	aca	att	gcc	aag	ctc	ggt	aag	tat	atg	tat	480
Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr	
145					150					155					160	
gac	aat	cgg	gaa	agt	caa	gat	acc	agc	ttt	act	acc	ttg	gtg	gag	aga	528
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg	
				165					170					175		
ggt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt	576
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	
			180					185					190			
cat	ttt	ccc	ggg	caa	gca	ggt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg	624
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	
		195					200					205				
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata	672
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile	
	210					215					220					

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ctc Leu 225	tac Tyr	aga Arg	aca Thr	gct Ala 230	agg Arg 230	act Thr	cag Gln	att Ile	gga Gly 235	tca Ser 235	aaa Lys	ttc Phe	aca Thr	cgg Arg	tgg Trp 240	720
gga Gly	tca Ser	cag Gln	gga Gly	gaa Glu 245	aga Arg	ggc Gly	aaa Lys	gac Asp	aag Lys 250	aaa Lys	gga Gly	agc Ser	tgc Cys	aat Asn 255	ctc Leu	768
tct Ser	cgt Arg	gtg Val	gac Asp 260	agc Ser	aca Thr	acc Thr	tgc Cys	ctt Leu 265	ttc Phe	ccg Pro	gtg Val	gaa Glu 270	gaa Glu 270	aaa Lys	gca Ala	816
gtg Val	gag Glu	tat Tyr 275	tac Tyr	ttt Phe	gct Ala	tct Ser	gat Asp 280	gca Ala	agt Ser	gct Ala	gtc Val	ata Ile 285	gaa Glu	cac His	acc Thr	864
aat Asn	cgc Arg 290	gtc Val	atc Ile	ttt Phe	ctg Leu	gaa Glu 295	gat Asp	gat Asp	gat Asp	gtt Val	gca Ala 300	gca Ala	gta Val	gtg Val	gat Asp	912
gga Gly 305	cgt Arg	ctt Leu	tct Ser	atc Ile	cat His 310	cga Arg	att Ile	aaa Lys	cga Arg	act Thr 315	gca Ala	gga Gly	gat Asp	cac His	ccc Pro 320	960
gga Gly	cga Arg	gct Ala	gtg Val	caa Gln 325	aca Thr	ctc Leu	cag Gln	atg Met	gaa Glu 330	ctc Leu	cag Gln	cag Gln	atc Ile	atg Met 335	aag Lys	1008
ggc Gly	aac Asn	ttc Phe	agt Ser 340	tca Ser	ttt Phe	atg Met	cag Gln	aag Lys 345	gaa Glu	ata Ile	ttt Phe	gag Glu	cag Gln 350	cca Pro	gag Glu	1056
tct Ser	gtc Val	gtg Val 355	aac Asn	aca Thr	atg Met	aga Arg	gga Gly 360	aga Arg	gtc Val	aac Asn	ttt Phe	gat Asp 365	gac Asp	tat Tyr	act Thr	1104
gtg Val	aat Asn 370	ttg Leu	ggt Gly	ggt Gly	ttg Leu	aag Lys 375	gat Asp	cac His	ata Ile	aag Lys	gag Glu 380	atc Ile	cag Gln	aga Arg	tgc Cys	1152
cgg Arg 385	cgt Arg	ttg Leu	att Ile	ctt Leu	att Ile 390	gct Ala	tgt Cys	gga Gly	aca Thr	agt Ser 395	tac Tyr	cat His	gct Ala	ggt Gly	gta Val 400	1200
gca Ala	aca Thr	cgt Arg	caa Gln	gtt Val 405	ctt Leu	gag Glu	gag Glu	ctg Leu	act Thr 410	gag Glu	ttg Leu	cct Pro	gtg Val 415	atg Met 415	gtg Val	1248
gaa Glu	cta Leu	gca Ala	agt Ser 420	gac Asp	ttc Phe	ctg Leu	gac Asp	aga Arg 425	aac Asn	aca Thr	cca Pro	gtc Val	ttt Phe 430	cga Arg	gat Asp	1296
gat Asp	gtt Val	tgc Cys 435	ttt Phe	ttc Phe	ctt Leu	agt Ser	caa Gln 440	tca Ser	ggt Gly	gag Glu	aca Thr	gca Ala 445	gat Asp	act Thr	ttg Leu	1344
atg Met	ggt Gly 450	ctt Leu	cgt Arg	tac Tyr	tgt Cys	aag Lys 455	gag Glu	aga Arg	gga Gly	gct Ala	tta Leu 460	act Thr	gtg Val	ggg Gly	atc Ile	1392

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aca Thr 465	aac Asn	aca Thr	gtt Val	ggc Gly	agt Ser 470	tcc Ser	ata Ile	tca Ser	cgg Arg 475	gag Glu	aca Thr	gat Asp	tgt Cys	gga Gly	gtt Val 480	1440
cat His	att Ile	aat Asn	gct Ala	ggt Gly 485	cct Pro	gag Glu	att Ile	ggt Gly	gtg Val 490	gcc Ala	agt Ser	aca Thr	aag Lys	gct Ala 495	tat Tyr	1488
acc Thr	agc Ser	cag Gln	ttt Phe 500	gta Val	tcc Ser	ctt Leu	gtg Val	atg Met 505	ttt Phe	gcc Ala	ctt Leu	atg Met 510	atg Met 510	tgt Cys	gat Asp	1536
gat Asp	cgg Arg	atc Ile 515	tcc Ser	atg Met	caa Gln	gaa Glu	aga Arg 520	cgc Arg	aaa Lys	gag Glu	atc Ile	atg Met 525	ctt Leu	gga Gly	ttg Leu	1584
aaa Lys	cgg Arg 530	ctg Leu	cct Pro	gat Asp	ttg Leu	att Ile 535	aag Lys	gaa Glu	gta Val	ctg Leu	agc Ser 540	atg Met	gat Asp	gac Asp	gaa Glu	1632
att Ile 545	cag Gln	aaa Lys	cta Leu	gca Ala	aca Thr 550	gaa Glu	ctt Leu	tat Tyr	cat His	cag Gln 555	aag Lys	tca Ser	gtt Val	ctg Leu	ata Ile 560	1680
atg Met	gga Gly	cga Arg	ggc Gly	tat Tyr 565	cat His	tat Tyr	gct Ala	act Thr	tgt Cys 570	ctt Leu	gaa Glu	ggg Gly	gca Ala	ctg Leu 575	aaa Lys	1728
atc Ile	aaa Lys	gaa Glu	att Ile 580	act Thr	tat Tyr	atg Met	cac His	tct Ser 585	gaa Glu	ggc Gly	atc Ile	ctt Leu	gct Ala 590	ggt Gly	gaa Glu	1776
ttg Leu	aaa Lys	cat His 595	ggc Gly	cct Pro	ctg Leu	gct Ala	ttg Leu 600	gtg Val	gat Asp	aaa Lys	ttg Leu	atg Met 605	cct Pro	gtg Val	atc Ile	1824
atg Met	atc Ile 610	atc Ile	atg Met	aga Arg	gat Asp	cac His 615	act Thr	tat Tyr	gcc Ala	aag Lys	tgt Cys 620	cag Gln	aat Asn	gct Ala	ctt Leu	1872
cag Gln 625	caa Gln	gtg Val	gtt Val	gct Ala	cgg Arg 630	cag Gln	ggg Gly	cgg Arg	cct Pro	gtg Val 635	gta Val	att Ile	tgt Cys	gat Asp	aag Lys 640	1920
gag Glu	gat Asp	act Thr	gag Glu	acc Thr 645	att Ile	aag Lys	aac Asn	aca Thr	aaa Lys 650	aga Arg	acg Thr	atc Ile	aag Lys	gtg Val 655	ccc Pro	1968
cac His	tca Ser	gtg Val	gac Asp 660	tgc Cys	ttg Leu	cag Gln	ggc Gly	att Ile 665	ctc Leu	agc Ser	gtg Val	atc Ile	cct Pro 670	tta Leu	cag Gln	2016
ttg Leu	ctg Leu	gct Ala 675	ttc Phe	cac His	ctt Leu	gct Ala	gtg Val 680	ctg Leu	aga Arg	ggc Gly	tat Tyr	gat Asp 685	gtt Val	gat Asp	ttc Phe	2064
cca Pro	cgg Arg 690	aat Asn	ctt Leu	gcc Ala	aaa Lys	tct Ser 695	gtg Val	act Thr	gta Val	gag Glu	tga					2100

GFAT-anglais

<210> 6
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (57)..(57)
 <223> 'Xaa' in position 57 represents Thr or Ile

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 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
 115 120 125
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
 130 135 140
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
 145 150 155 160
 Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
 165 170 175
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
 180 185 190
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
 195 200 205
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
 210 215 220
 Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp
 225 230 235 240
 Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu
 245 250 255
 Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala
 260 265 270
 Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr

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275					280					285					
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp
	290					295					300				
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	Asp	His	Pro
305					310					315					320
Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	Leu	Gln	Gln	Ile	Met	Lys
				325					330					335	
Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	Ile	Phe	Glu	Gln	Pro	Glu
			340					345					350		
Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	Phe	Asp	Asp	Tyr	Thr
		355					360					365			
Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	Lys	Glu	Ile	Gln	Arg	Cys
	370					375					380				
Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	Ser	Tyr	His	Ala	Gly	Val
385					390					395					400
Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	Pro	Val	Met	Val
				405					410					415	
Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	Val	Phe	Arg	Asp
				420					425					430	
Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Thr	Leu
		435					440					445			
Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu	Thr	Val	Gly	Ile
	450					455					460				
Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val
465					470					475					480
His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr
				485					490					495	
Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu	Met	Met	Cys	Asp
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Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys	Glu	Ile	Met	Leu	Gly	Leu
		515					520					525			
Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	Leu	Ser	Met	Asp	Asp	Glu
	530					535					540				
Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys	Ser	Val	Leu	Ile
545					550					555					560
Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys
				565					570					575	
Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu
			580					585					590		
Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	Met	Pro	Val	Ile
		595					600					605			

GFAT-anglais

Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu
610 615 620
Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys
625 630 635 640
Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro
645 650 655
His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln
660 665 670
Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe
675 680 685
Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
690 695

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<212> DNA
<213> Artificial sequence

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cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac 96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
20 25 30
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa 144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
35 40 45
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga 192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
50 55 60
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat 240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
65 70 75 80
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg 288

									GFAT-anglais							
Leu	Asp	Ile	Glu	Phe 85	Asp	Val	His	Leu	Gly 90	Ile	Ala	His	Thr	Arg 95	Trp	
gca Ala	aca Thr	cat His	gga Gly 100	gaa Glu	ccc Pro	agt Ser	cct Pro	gtc Val 105	aat Asn	agc Ser	cac His	ccc Pro	cag Gln 110	cgc Arg	tct Ser	336
gat Asp	aaa Lys	aat Asn 115	aat Asn	gaa Glu	ttt Phe	atc Ile	gtt Val 120	att Ile	cac His	aat Asn	gga Gly	atc Ile 125	atc Ile	acc Thr	aac Asn	384
tac Tyr	aaa Lys 130	gac Asp	ttg Leu	aaa Lys	aag Lys	ttt Phe 135	ttg Leu	gaa Glu	agc Ser	aaa Lys	ggc Gly 140	tat Tyr	gac Asp	ttc Phe	gaa Glu	432
tct Ser 145	gaa Glu	aca Thr	gac Asp	aca Thr	gag Glu 150	aca Thr	att Ile	gcc Ala	aag Lys	ctc Leu 155	gtt Val	aag Lys	tat Tyr	atg Met	tat Tyr 160	480
gac Asp	aat Asn	cgg Arg	gaa Glu	agt Ser 165	caa Gln	gat Asp	acc Thr	agc Ser	ttt Phe 170	act Thr	acc Thr	ttg Leu	gtg Val	gag Glu 175	aga Arg	528
gtt Val	atc Ile	caa Gln 180	caa Gln	ttg Leu	gaa Glu	ggg Gly	gct Ala	ttt Phe 185	gca Ala	ctt Leu	gtg Val	ttt Phe 190	aaa Lys	agt Ser	gtt Val	576
cat His	ttt Phe	ccc Pro 195	ggg Gly	caa Gln	gca Ala	gtt Val	ggc Gly 200	aca Thr	agg Arg	cga Arg	ggg Gly	agc Ser 205	cct Pro	ctg Leu	ttg Leu	624
att Ile	ggg Gly 210	gta Val	cgg Arg	agt Ser	gaa Glu	cat His 215	aaa Lys	ctt Leu	tct Ser	act Thr	gat Asp 220	cac His	att Ile	cct Pro	ata Ile	672
ctc Leu 225	tac Tyr	aga Arg	aca Thr	ggc Gly	aaa Lys 230	gac Asp	aag Lys	aaa Lys	gga Gly	agc Ser 235	tgc Cys	aat Asn	ctc Leu	tct Ser	cgt Arg 240	720
gtg Val	gac Asp	agc Ser	aca Thr	acc Thr 245	tgc Cys	ctt Leu	ttc Phe	ccg Pro	gtg Val 250	gaa Glu	gaa Glu	aaa Lys	gca Ala	gtg Val 255	gag Glu	768
tat Tyr	tac Tyr	ttt Phe	gct Ala 260	tct Ser	gat Asp	gca Ala	agt Ser	gct Ala 265	gtc Val	ata Ile	gaa Glu	cac His	acc Thr 270	aat Asn	cgc Arg	816
gtc Val	atc Ile	ttt Phe 275	ctg Leu	gaa Glu	gat Asp	gat Asp	gat Asp 280	gtt Val	gca Ala	gca Ala	gta Val	gtg Val 285	gat Asp	gga Gly	cgt Arg	864
ctt Leu	tct Ser 290	atc Ile	cat His	cga Arg	att Ile	aaa Lys 295	cga Arg	act Thr	gca Ala	gga Gly	cat His 300	cac His	cat His	cac His	cat His	912
cac His 305	gat Asp	cac His	ccc Pro	gga Gly	cga Arg 310	gct Ala	gtg Val	caa Gln	aca Thr	ctc Leu 315	cag Gln	atg Met	gaa Glu	ctc Leu	cag Gln 320	960
cag Gln	atc Ile	atg Met	aag Lys	ggc Gly 325	aac Asn	ttc Phe	agt Ser	tca Ser	ttt Phe 330	atg Met	cag Gln	aag Lys	gaa Glu	ata Ile 335	ttt Phe	1008

GFAT-anglais																
gag Glu	cag Gln	cca Pro	gag Glu 340	tct Ser	gtc Val	gtg Val	aac Asn	aca Thr 345	atg Met	aga Arg	gga Gly	aga Arg	gtc Val 350	aac Asn	ttt Phe	1056
gat Asp	gac Asp	tat Tyr 355	act Thr	gtg Val	aat Asn	ttg Leu	ggt Gly 360	ggt Gly	ttg Leu	aag Lys	gat Asp	cac His 365	ata Ile	aag Lys	gag Glu	1104
atc Ile	cag Gln 370	aga Arg	tgc Cys	cgg Arg	cgt Arg	ttg Leu 375	att Ile	ctt Leu	att Ile	gct Ala	tgt Cys 380	gga Gly	aca Thr	agt Ser	tac Tyr	1152
cat His 385	gct Ala	ggt Gly	gta Val	gca Ala	aca Thr 390	cgt Arg	caa Gln	ggt Val	ctt Leu	gag Glu 395	gag Glu	ctg Leu	act Thr	gag Glu	ttg Leu 400	1200
cct Pro	gtg Val	atg Met	gtg Val	gaa Glu 405	cta Leu	gca Ala	agt Ser	gac Asp	ttc Phe 410	ctg Leu	gac Asp	aga Arg	aac Asn	aca Thr 415	cca Pro	1248
gtc Val	ttt Phe	cga Arg	gat Asp 420	gat Asp	gtt Val	tgc Cys	ttt Phe	ttc Phe 425	ctt Leu	agt Ser	caa Gln	tca Ser	ggt Gly 430	gag Glu	aca Thr	1296
gca Ala	gat Asp	act Thr 435	ttg Leu	atg Met	ggt Gly	ctt Leu	cgt Arg 440	tac Tyr	tgt Cys	aag Lys	gag Glu	aga Arg 445	gga Gly	gct Ala	tta Leu	1344
act Thr	gtg Val 450	ggg Gly	atc Ile	aca Thr	aac Asn	aca Thr 455	ggt Val	ggc Gly	agt Ser	tcc Ser	ata Ile 460	tca Ser	cgg Arg	gag Glu	aca Thr	1392
gat Asp 465	tgt Cys	gga Gly	gtt Val	cat His	att Ile 470	aat Asn	gct Ala	ggt Gly	cct Pro	gag Glu 475	att Ile	ggt Gly	gtg Val	gcc Ala	agt Ser 480	1440
aca Thr	aag Lys	gct Ala	tat Tyr	acc Thr 485	agc Ser	cag Gln	ttt Phe	gta Val	tcc Ser 490	ctt Leu	gtg Val	atg Met	ttt Phe	gcc Ala 495	ctt Leu	1488
atg Met	atg Met	tgt Cys	gat Asp 500	gat Asp	cgg Arg	atc Ile	tcc Ser	atg Met 505	caa Gln	gaa Glu	aga Arg	cgc Arg	aaa Lys 510	gag Glu	atc Ile	1536
atg Met	ctt Leu	gga Gly 515	ttg Leu	aaa Lys	cgg Arg	ctg Leu	cct Pro 520	gat Asp	ttg Leu	att Ile	aag Lys	gaa Glu 525	gta Val	ctg Leu	agc Ser	1584
atg Met	gat Asp 530	gac Asp	gaa Glu	att Ile	cag Gln	aaa Lys 535	cta Leu	gca Ala	aca Thr	gaa Glu	ctt Leu 540	tat Tyr	cat His	cag Gln	aag Lys	1632
tca Ser 545	gtt Val	ctg Leu	ata Ile	atg Met	gga Gly 550	cga Arg	ggc Gly	tat Tyr	cat His	tat Tyr 555	gct Ala	act Thr	tgt Cys	ctt Leu	gaa Glu 560	1680
ggg Gly	gca Ala	ctg Leu	aaa Lys	atc Ile 565	aaa Lys	gaa Glu	att Ile	act Thr	tat Tyr 570	atg Met	cac His	tct Ser	gaa Glu	ggc Gly 575	atc Ile	1728
ctt	gct	ggt	gaa	ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg	1776

GFAT-anglais

Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	
			580					585					590			
atg	cct	gtg	atc	atg	atc	atc	atg	aga	gat	cac	act	tat	gcc	aag	tgt	1824
Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	
		595					600					605				
cag	aat	gct	ctt	cag	caa	gtg	gtt	gct	cgg	cag	ggg	cgg	cct	gtg	gta	1872
Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	
	610					615					620					
att	tgt	gat	aag	gag	gat	act	gag	acc	att	aag	aac	aca	aaa	aga	acg	1920
Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	
	625				630					635					640	
atc	aag	gtg	ccc	cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	1968
Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	
				645					650					655		
atc	cct	tta	cag	ttg	ctg	gct	ttc	cac	ctt	gct	gtg	ctg	aga	ggc	tat	2016
Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	
			660					665					670			
gat	gtt	gat	ttc	cca	cgg	aat	ctt	gcc	aaa	tct	gtg	act	gta	gag	tga	2064
Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu		
		675					680					685				

<210> 8
 <211> 687
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (57)..(57)
 <223> 'Xaa' in position 57 represents Thr or Ile

<220>
 <223> modified GFAT1 by an internal purification tag

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 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
 20 25 30
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110

GFAT-anglais

Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
115 120 125

Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
130 135 140

Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
145 150 155 160

Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
165 170 175

Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
180 185 190

His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
195 200 205

Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
210 215 220

Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg
225 230 235 240

Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu
245 250 255

Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg
260 265 270

Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg
275 280 285

Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly His His His His His
290 295 300

His Asp His Pro Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln
305 310 315 320

Gln Ile Met Lys Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe
325 330 335

Glu Gln Pro Glu Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe
340 345 350

Asp Asp Tyr Thr Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu
355 360 365

Ile Gln Arg Cys Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr
370 375 380

His Ala Gly Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu
385 390 395 400

Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro
405 410 415

Val Phe Arg Asp Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr
420 425 430

Ala Asp Thr Leu Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu

GFAT-anglais

435 440 445

Thr Val Gly Ile Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr
450 455 460

Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser
465 470 475 480

Thr Lys Ala Tyr Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu
485 490 495

Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile
500 505 510

Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser
515 520 525

Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys
530 535 540

Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu
545 550 555 560

Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile
565 570 575

Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu
580 585 590

Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys
595 600 605

Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val
610 615 620

Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr
625 630 635 640

Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val
645 650 655

Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr
660 665 670

Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
675 680 685

<210> 9
<211> 2067
<212> DNA
<213> Artificial sequence

<220>
<223> modified GFAT2 by an internal purification tag

<220>
<221> CDS
<222> (1)..(2067)
<223>

<400> 9

GFAT-anglais																
atg tgc gga atc ttt gcc tac atg aac tac aga gtc ccc cgg acg agg Met Cys Gly Ile Phe Ala Tyr Met Asn Tyr Arg Val Pro Arg Thr Arg 1 5 10 15																48
aag gag atc ttc gaa acc ctc atc aag ggc ctg cag cgg ctg gag tac Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr 20 25 30																96
aga ggc tac gac tcg gca ggt gtg gcg atc gat ggg aat aat cac gaa Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu 35 40 45																144
gtc aaa gaa aga cac att cag ctg gtc aag aaa agg ggg aaa gtc aag Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys 50 55 60																192
gct ctc gat gaa gaa ctt tac aaa caa gac agc atg gac tta aaa gtg Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val 65 70 75 80																240
gag ttt gag aca cac ttc ggc att gcc cac acg cgc tgg gcc acc cac Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His 85 90 95																288
ggg gtc ccc agt gct gtc aac agc cac cct cag cgc tca gac aaa ggc Gly Val Pro Ser Ala Val Asn Ser His Pro Gln Arg Ser Asp Lys Gly 100 105 110																336
aac gaa ttt gtt gtc atc cac aat ggg atc atc aca aat tac aaa gat Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp 115 120 125																384
ctg agg aaa ttt ctg gaa agc aaa ggc tac gag ttt gag tca gaa aca Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr 130 135 140																432
gat aca gag acc atc gcc aag ctg att aaa tat gtg ttc gac aac aga Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg 145 150 155 160																480
gaa act gag gac att acg ttt tca acg ttg gtc gag aga gtc att cag Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln 165 170 175																528
cag ttg gaa ggt gca ttc gcg ctg gtt ttc aag agt gtc cac tac cca Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro 180 185 190																576
gga gaa gcc gtt gcc aca cgg aga ggc agc ccc ctg ctc atc gga gtc Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val 195 200 205																624
cgg agc aaa tac aag ctc tcc aca gaa cag atc cct atc tta tac agg Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg 210 215 220																672
acg tgc act ctg gag aat gtg aag aat atc tgt aag aca cgg atg aag Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys 225 230 235 240																720
agg ctg gac agc tcc gcc tgc ctg cat gct gtg ggc gac aag gcc gtg Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val 245 250 255																768

GFAT-anglais

gaa Glu	ttc Phe	ttc Phe	ttt Phe 260	gct Ala	tct Ser	gat Asp	gca Ala	agc Ser 265	gct Ala	atc Ile	ata Ile	gag Glu	cac His 270	acc Thr	aac Asn	816
cgg Arg	gtc Val	atc Ile 275	ttc Phe	ctg Leu	gag Glu	gac Asp	gat Asp 280	gac Asp	atc Ile	gcc Ala	gca Ala	gtg Val 285	gct Ala	gat Asp	ggg Gly	864
aaa Lys	ctc Leu 290	tcc Ser	att Ile	cac His	cgg Arg	gtc Val 295	aag Lys	cgc Arg	tcg Ser	gcc Ala	agt Ser 300	cat His	cac His	cat His	cac His	912
cat His 305	cac His	gat Asp	gac Asp	cca Pro	tct Ser 310	cga Arg	gcc Ala	atc Ile	cag Gln	acc Thr 315	ttg Leu	cag Gln	atg Met	gaa Glu	ctg Leu 320	960
cag Gln	caa Gln	atc Ile	atg Met	aaa Lys 325	ggt Gly	aac Asn	ttc Phe	agt Ser	gcg Ala 330	ttt Phe	atg Met	cag Gln	aag Lys	gag Glu 335	atc Ile	1008
ttc Phe	gaa Glu	cag Gln	cca Pro 340	gaa Glu	tca Ser	gtt Val	ttc Phe	aat Asn 345	act Thr	atg Met	aga Arg	ggt Gly	cgg Arg 350	gtg Val	aat Asn	1056
ttt Phe	gaa Glu	acc Thr 355	aac Asn	aca Thr	gtg Val	ctc Leu	ctg Leu 360	ggt Gly	ggc Gly	ttg Leu	aag Lys	gac Asp 365	cac His	ttg Leu	aag Lys	1104
gag Glu	att Ile 370	cga Arg	cga Arg	tgc Cys	cga Arg	cgg Arg 375	ctc Leu	atc Ile	gtg Val	att Ile	ggc Gly 380	tgt Cys	gga Gly	acc Thr	agc Ser	1152
tac Tyr 385	cac His	gct Ala	gcc Ala	gtg Val	gct Ala 390	acg Thr	cgg Arg	caa Gln	gtt Val	ttg Leu 395	gag Glu	gaa Glu	ctg Leu	act Thr	gag Glu 400	1200
ctt Leu	cct Pro	gtg Val	atg Met	gtt Val 405	gaa Glu	ctt Leu	gct Ala	agt Ser	gat Asp 410	ttt Phe	ctg Leu	gac Asp	agg Arg	aac Asn 415	aca Thr	1248
cct Pro	gtg Val	ttc Phe	agg Arg 420	gat Asp	gac Asp	gtt Val	tgc Cys	ttt Phe 425	ttc Phe	atc Ile	agc Ser	cag Gln	tca Ser 430	ggc Gly	gag Glu	1296
acc Thr	gcg Ala	gac Asp 435	acc Thr	ctc Leu	ctg Leu	gcg Ala	ctg Leu 440	cgc Arg	tac Tyr	tgt Cys	aag Lys	gac Asp 445	cgc Arg	ggc Gly	gct Ala	1344
ctc Leu	acc Thr 450	gtg Val	ggc Gly	gtc Val	acc Thr	aac Asn 455	acc Thr	gtg Val	ggc Gly	agc Ser	tcc Ser 460	atc Ile	tct Ser	cgc Arg	gag Glu	1392
acc Thr 465	gac Asp	tgc Cys	ggc Gly	gtc Val	cac His 470	atc Ile	aac Asn	gca Ala	ggg Gly	ccg Pro 475	gag Glu	gtc Val	ggc Gly	gtg Val	gcc Ala 480	1440
agc Ser	acc Thr	aag Lys	gct Ala 485	tat Tyr	acc Thr	agt Ser	cag Gln	ttc Phe	atc Ile 490	tct Ser	ctg Leu	gtg Val	atg Met	ttt Phe 495	ggt Gly	1488
ttg Leu	atg Met	atg Met	tct Ser	gaa Glu	gac Asp	cga Arg	att Ile	tca Ser	cta Leu	caa Gln	aac Asn	agg Arg	agg Arg	caa Gln	gag Glu	1536

GFAT-anglais																
500				505				510								
atc	atc	cgt	ggc	ttg	aga	tct	tta	cct	gag	ctg	atc	aag	gaa	gtg	ctg	1584
Ile	Ile	Arg	Gly	Leu	Arg	Ser	Leu	Pro	Glu	Leu	Ile	Lys	Glu	Val	Leu	
		515					520					525				
tct	ctg	gag	gag	aag	atc	cac	gac	ttg	gcc	ctg	gag	ctc	tac	acg	cag	1632
Ser	Leu	Glu	Glu	Lys	Ile	His	Asp	Leu	Ala	Leu	Glu	Leu	Tyr	Thr	Gln	
	530					535					540					
aga	tcg	ctg	ctg	gtg	atg	ggg	cgg	ggc	tac	aac	tat	gcc	acc	tgc	ctg	1680
Arg	Ser	Leu	Leu	Val	Met	Gly	Arg	Gly	Tyr	Asn	Tyr	Ala	Thr	Cys	Leu	
545					550					555					560	
gaa	gga	gcc	ctg	aaa	att	aaa	gag	ata	acc	tac	atg	cac	tca	gaa	ggc	1728
Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	
				565					570					575		
atc	ctg	gct	ggg	gag	ctg	aag	cac	ggg	ccc	ctg	gca	ctg	att	gac	aag	1776
Ile	Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp	Lys	
			580					585					590			
cag	atg	ccc	gtc	atc	atg	gtc	att	atg	aag	gat	cct	tgc	ttc	gcc	aaa	1824
Gln	Met	Pro	Val	Ile	Met	Val	Ile	Met	Lys	Asp	Pro	Cys	Phe	Ala	Lys	
		595					600					605				
tgc	cag	aac	gcc	ctg	cag	caa	gtc	acg	gcc	cgc	cag	ggt	cgc	ccc	att	1872
Cys	Gln	Asn	Ala	Leu	Gln	Gln	Val	Thr	Ala	Arg	Gln	Gly	Arg	Pro	Ile	
	610					615					620					
ata	ctg	tgc	tcc	aag	gac	gat	act	gaa	agt	tcc	aag	ttt	gcg	tat	aag	1920
Ile	Leu	Cys	Ser	Lys	Asp	Asp	Thr	Glu	Ser	Ser	Lys	Phe	Ala	Tyr	Lys	
625					630					635					640	
aca	atc	gag	ctg	ccc	cac	act	gtg	gac	tgc	ctc	cag	ggc	atc	ctg	agc	1968
Thr	Ile	Glu	Leu	Pro	His	Thr	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	
				645					650					655		
gtg	att	ccg	ctg	cag	ctg	ctg	tcc	ttc	cac	ctg	gct	gtt	ctc	cga	gga	2016
Val	Ile	Pro	Leu	Gln	Leu	Leu	Ser	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	
			660					665					670			
tat	gac	gtt	gac	ttc	ccc	aga	aat	ctg	gcc	aag	tct	gta	act	gtg	gaa	2064
Tyr	Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu	
		675					680					685				
tga																2067

<210> 10
 <211> 688
 <212> PRT
 <213> Artificial sequence

<220>
 <223> modified GFAT2 by an internal purification tag

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 Met Cys Gly Ile Phe Ala Tyr Met Asn Tyr Arg Val Pro Arg Thr Arg
 1 5 10 15

Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr

GFAT-anglais

20					25					30					
Arg	Gly	Tyr ₃₅	Asp	Ser	Ala	Gly	Val ₄₀	Ala	Ile	Asp	Gly	Asn ₄₅	Asn	His	Glu
Val	Lys ₅₀	Glu	Arg	His	Ile	Gln ₅₅	Leu	Val	Lys	Lys	Arg ₆₀	Gly	Lys	Val	Lys
Ala ₆₅	Leu	Asp	Glu	Glu	Leu ₇₀	Tyr	Lys	Gln	Asp	Ser ₇₅	Met	Asp	Leu	Lys	Val ₈₀
Glu	Phe	Glu	Thr	His ₈₅	Phe	Gly	Ile	Ala	His ₉₀	Thr	Arg	Trp	Ala	Thr ₉₅	His
Gly	Val	Pro	Ser ₁₀₀	Ala	Val	Asn	Ser	His ₁₀₅	Pro	Gln	Arg	Ser	Asp ₁₁₀	Lys	Gly
Asn	Glu	Phe ₁₁₅	Val	Val	Ile	His	Asn ₁₂₀	Gly	Ile	Ile	Thr	Asn ₁₂₅	Tyr	Lys	Asp
Leu	Arg ₁₃₀	Lys	Phe	Leu	Glu	Ser ₁₃₅	Lys	Gly	Tyr	Glu	Phe ₁₄₀	Glu	Ser	Glu	Thr
Asp ₁₄₅	Thr	Glu	Thr	Ile	Ala ₁₅₀	Lys	Leu	Ile	Lys	Tyr ₁₅₅	Val	Phe	Asp	Asn	Arg ₁₆₀
Glu	Thr	Glu	Asp	Ile ₁₆₅	Thr	Phe	Ser	Thr	Leu ₁₇₀	Val	Glu	Arg	Val	Ile ₁₇₅	Gln
Gln	Leu	Glu	Gly ₁₈₀	Ala	Phe	Ala	Leu	Val ₁₈₅	Phe	Lys	Ser	Val	His ₁₉₀	Tyr	Pro
Gly	Glu	Ala ₁₉₅	Val	Ala	Thr	Arg	Arg ₂₀₀	Gly	Ser	Pro	Leu	Leu ₂₀₅	Ile	Gly	Val
Arg	Ser ₂₁₀	Lys	Tyr	Lys	Leu	Ser ₂₁₅	Thr	Glu	Gln	Ile	Pro ₂₂₀	Ile	Leu	Tyr	Arg
Thr ₂₂₅	Cys	Thr	Leu	Glu	Asn ₂₃₀	Val	Lys	Asn	Ile	Cys ₂₃₅	Lys	Thr	Arg	Met	Lys ₂₄₀
Arg	Leu	Asp	Ser	Ser ₂₄₅	Ala	Cys	Leu	His	Ala ₂₅₀	Val	Gly	Asp	Lys	Ala ₂₅₅	Val
Glu	Phe	Phe	Phe ₂₆₀	Ala	Ser	Asp	Ala	Ser ₂₆₅	Ala	Ile	Ile	Glu	His ₂₇₀	Thr	Asn
Arg	Val	Ile ₂₇₅	Phe	Leu	Glu	Asp	Asp ₂₈₀	Asp	Ile	Ala	Ala	Val ₂₈₅	Ala	Asp	Gly
Lys	Leu ₂₉₀	Ser	Ile	His	Arg	Val ₂₉₅	Lys	Arg	Ser	Ala	Ser ₃₀₀	His	His	His	His
His ₃₀₅	His	Asp	Asp	Pro	Ser ₃₁₀	Arg	Ala	Ile	Gln	Thr ₃₁₅	Leu	Gln	Met	Glu	Leu ₃₂₀
Gln	Gln	Ile	Met	Lys ₃₂₅	Gly	Asn	Phe	Ser	Ala ₃₃₀	Phe	Met	Gln	Lys	Glu ₃₃₅	Ile
Phe	Glu	Gln	Pro ₃₄₀	Glu	Ser	Val	Phe	Asn ₃₄₅	Thr	Met	Arg	Gly	Arg ₃₅₀	Val	Asn
Phe	Glu	Thr	Asn	Thr	Val	Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys

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355		360		365
Glu Ile Arg Arg Cys Arg Arg	Leu Ile Val Ile Gly Cys Gly Thr Ser			
370	375	380		
Tyr His Ala Ala Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu				
385	390	395		400
Leu Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr				
	405	410		415
Pro Val Phe Arg Asp Asp Val Cys Phe Phe Ile Ser Gln Ser Gly Glu				
	420	425		430
Thr Ala Asp Thr Leu Leu Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala				
	435	440		445
Leu Thr Val Gly Val Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu				
	450	455		460
Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Val Gly Val Ala				
	465	470		475
Ser Thr Lys Ala Tyr Thr Ser Gln Phe Ile Ser Leu Val Met Phe Gly				
	485	490		495
Leu Met Met Ser Glu Asp Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu				
	500	505		510
Ile Ile Arg Gly Leu Arg Ser Leu Pro Glu Leu Ile Lys Glu Val Leu				
	515	520		525
Ser Leu Glu Glu Lys Ile His Asp Leu Ala Leu Glu Leu Tyr Thr Gln				
	530	535		540
Arg Ser Leu Leu Val Met Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu				
	545	550		555
Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly				
	565	570		575
Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Lys				
	580	585		590
Gln Met Pro Val Ile Met Val Ile Met Lys Asp Pro Cys Phe Ala Lys				
	595	600		605
Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile				
	610	615		620
Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys				
	625	630		635
Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser				
	645	650		655
Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly				
	660	665		670
Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu				
	675	680		685

GFAT-anglais

<210> 11
 <211> 2118
 <212> DNA
 <213> Artificial sequence

<220>
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 <221> CDS
 <222> (1)..(2118)
 <223>

<220>
 <221> misc_feature
 <222> (170)..(170)
 <223> t or c

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cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac	96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr	
20 25 30	
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa	144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Asn Asp Lys	
35 40 45	
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga	192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly	
50 55 60	
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat	240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp	
65 70 75 80	
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg	288
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp	
85 90 95	
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct	336
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser	
100 105 110	
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac	384
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn	
115 120 125	
tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa	432
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu	
130 135 140	
tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat	480
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr	
145 150 155 160	
gac aat cgg gaa agt caa gat acc agc ttt act acc ttg gtg gag aga	528

GFAT-anglais															
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg
				165					170					175	
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val
			180					185					190		
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu
		195					200					205			
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile
	210					215					220				
ctc	tac	aga	aca	gct	agg	act	cag	att	gga	tca	aaa	ttc	aca	cgg	tgg
Leu	Tyr	Arg	Thr	Ala	Arg	Thr	Gln	Ile	Gly	Ser	Lys	Phe	Thr	Arg	Trp
					230				235						240
gga	tca	cag	gga	gaa	aga	ggc	aaa	gac	aag	aaa	gga	agc	tgc	aat	ctc
Gly	Ser	Gln	Gly	Glu	Arg	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu
				245				250						255	
tct	cgt	gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca
Ser	Arg	Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala
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gtg	gag	tat	tac	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc
Val	Glu	Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr
		275					280					285			
aat	cgc	gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp
	290					295					300				
gga	cgt	ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His
					310					315					320
cac	cat	cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa
His	His	His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu
				325					330					335	
ctc	cag	cag	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa
Leu	Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu
				340				345					350		
ata	ttt	gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc
Ile	Phe	Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val
		355					360					365			
aac	ttt	gat	gac	tat	act	gtg	aat	ttg	ggt	ggt	ttg	aag	gat	cac	ata
Asn	Phe	Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile
	370					375					380				
aag	gag	atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca
Lys	Glu	Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr
					390				395						400
agt	tac	cat	gct	ggg	gta	gca	aca	cgt	caa	gtt	ctt	gag	gag	ctg	act
Ser	Tyr	His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr
				405					410					415	

GFAT-anglais

gag Glu	ttg Leu	cct Pro	gtg Val 420	atg Met	gtg Val	gaa Glu	cta Leu	gca Ala 425	agt Ser	gac Asp	ttc Phe	ctg Leu	gac Asp 430	aga Arg	aac Asn	1296
aca Thr	cca Pro	gtc Val 435	ttt Phe	cga Arg	gat Asp	gat Asp	gtt Val 440	tgc Cys	ttt Phe	ttc Phe	ctt Leu	agt Ser 445	caa Gln	tca Ser	ggg Gly	1344
gag Glu	aca Thr 450	gca Ala	gat Asp	act Thr	ttg Leu	atg Met 455	ggg Gly	ctt Leu	cgt Arg	tac Tyr	tgt Cys 460	aag Lys	gag Glu	aga Arg	gga Gly	1392
gct Ala 465	tta Leu	act Thr	gtg Val	ggg Gly	atc Ile 470	aca Thr	aac Asn	aca Thr	gtt Val	ggc Gly 475	agt Ser	tcc Ser	ata Ile	tca Ser	cgg Arg 480	1440
gag Glu	aca Thr	gat Asp	tgt Cys	gga Gly 485	gtt Val	cat His	att Ile	aat Asn	gct Ala 490	ggg Gly	cct Pro	gag Glu	att Ile	ggg Gly 495	gtg Val	1488
gcc Ala	agt Ser	aca Thr	aag Lys 500	gct Ala	tat Tyr	acc Thr	agc Ser	cag Gln 505	ttt Phe	gta Val	tcc Ser	ctt Leu	gtg Val 510	atg Met	ttt Phe	1536
gcc Ala	ctt Leu	atg Met 515	atg Met	tgt Cys	gat Asp	gat Asp	cgg Arg 520	atc Ile	tcc Ser	atg Met	caa Gln	gaa Glu 525	aga Arg	cgc Arg	aaa Lys	1584
gag Glu	atc Ile 530	atg Met	ctt Leu	gga Gly	ttg Leu	aaa Lys 535	cgg Arg	ctg Leu	cct Pro	gat Asp	ttg Leu 540	att Ile	aag Lys	gaa Glu	gta Val	1632
ctg Leu 545	agc Ser	atg Met	gat Asp	gac Asp	gaa Glu 550	att Ile	cag Gln	aaa Lys	cta Leu	gca Ala 555	aca Thr	gaa Glu	ctt Leu	tat Tyr	cat His 560	1680
cag Gln	aag Lys	tca Ser	gtt Val	ctg Leu 565	ata Ile	atg Met	gga Gly	cga Arg	ggc Gly 570	tat Tyr	cat His	tat Tyr	gct Ala	act Thr 575	tgt Cys	1728
ctt Leu	gaa Glu	ggg Gly	gca Ala 580	ctg Leu	aaa Lys	atc Ile	aaa Lys	gaa Glu 585	att Ile	act Thr	tat Tyr	atg Met	cac His 590	tct Ser	gaa Glu	1776
ggc Gly	atc Ile	ctt Leu 595	gct Ala	ggg Gly	gaa Glu	ttg Leu	aaa Lys 600	cat His	ggc Gly	cct Pro	ctg Leu	gct Ala 605	ttg Leu	gtg Val	gat Asp	1824
aaa Lys	ttg Leu 610	atg Met	cct Pro	gtg Val	atc Ile	atg Met 615	atc Ile	atc Ile	atg Met	aga Arg	gat Asp 620	cac His	act Thr	tat Tyr	gcc Ala	1872
aag Lys 625	tgt Cys	cag Gln	aat Asn	gct Ala	ctt Leu 630	cag Gln	caa Gln	gtg Val	gtt Val	gct Ala 635	cgg Arg	cag Gln	ggg Gly	cgg Arg	cct Pro 640	1920
gtg Val	gta Val	att Ile	tgt Cys	gat Asp 645	aag Lys	gag Glu	gat Asp	act Thr	gag Glu 650	acc Thr	att Ile	aag Lys	aac Asn	aca Thr 655	aaa Lys	1968
aga Arg	acg Thr	atc Ile	aag Lys	gtg Val	ccc Pro	cac His	tca Ser	gtg Val	gac Asp	tgc Cys	ttg Leu	cag Gln	ggc Gly	att Ile	ctc Leu	2016

GFAT-anglais

660					665					670						
agc	gtg	atc	cct	tta	cag	ttg	ctg	gct	ttc	cac	ctt	gct	gtg	ctg	aga	2064
Ser	Val	Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	
		675					680					685				
ggc	tat	gat	gtt	gat	ttc	cca	cgg	aat	ctt	gcc	aaa	tct	gtg	act	gta	2112
Gly	Tyr	Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	
	690					695					700					
gag	tga															2118
Glu																
705																

<210> 12
 <211> 705
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (57)..(57)
 <223> 'xaa' in position 57 represents Thr or Ile

<220>
 <223> modified GFAT1Alt by an internal purification tag

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	Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr
			20						25					30		
	Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys
			35					40					45			
	Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly
		50					55					60				
	Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp
		65				70					75					80
	Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp
				85						90					95	
	Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser
				100					105					110		
	Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn
			115					120					125			
	Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu
		130					135					140				
	Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr
		145				150					155					160
	Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg
				165						170					175	
	Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val

190

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515 520 525
 Glu Ile Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val
 530 535 540
 Leu Ser Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His
 545 550 555 560
 Gln Lys Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys
 565 570 575
 Leu Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu
 580 585 590
 Gly Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp
 595 600 605
 Lys Leu Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala
 610 615 620
 Lys Cys Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro
 625 630 635 640
 Val Val Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys
 645 650 655
 Arg Thr Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu
 660 665 670
 Ser Val Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg
 675 680 685
 Gly Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 690 695 700
 Glu
 705

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 <211> 608
 <212> PRT
 <213> Escherichia coli

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 Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg Leu
 35 40 45
 Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu His
 50 55 60
 Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu Pro
 65 70 75 80
 Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val Val
 85 90 95

GFAT-anglais

His	Asn	Gly	Ile	Ile	Glu	Asn	His	Glu	Pro	Leu	Arg	Glu	Glu	Leu	Lys
			100					105					110		
Ala	Arg	Gly	Tyr	Thr	Phe	Val	Ser	Glu	Thr	Asp	Thr	Glu	Val	Ile	Ala
		115					120					125			
His	Leu	Val	Asn	Trp	Glu	Leu	Lys	Gln	Gly	Gly	Thr	Leu	Arg	Glu	Ala
	130					135					140				
Val	Leu	Arg	Ala	Ile	Pro	Gln	Leu	Arg	Gly	Ala	Tyr	Gly	Thr	Val	Ile
145					150					155					160
Met	Asp	Ser	Arg	His	Pro	Asp	Thr	Leu	Leu	Ala	Ala	Arg	Ser	Gly	Ser
				165					170					175	
Pro	Leu	Val	Ile	Gly	Leu	Gly	Met	Gly	Glu	Asn	Phe	Ile	Ala	Ser	Asp
			180					185					190		
Gln	Leu	Ala	Leu	Leu	Pro	Val	Thr	Arg	Arg	Phe	Ile	Phe	Leu	Glu	Glu
		195					200					205			
Gly	Asp	Ile	Ala	Glu	Ile	Thr	Arg	Arg	Ser	Val	Asn	Ile	Phe	Asp	Lys
	210					215					220				
Thr	Gly	Ala	Glu	Val	Lys	Arg	Gln	Asp	Ile	Glu	Ser	Asn	Leu	Gln	Tyr
225					230					235					240
Asp	Ala	Gly	Asp	Lys	Gly	Ile	Tyr	Arg	His	Tyr	Met	Gln	Lys	Glu	Ile
				245					250					255	
Tyr	Glu	Gln	Pro	Asn	Ala	Ile	Lys	Asn	Thr	Leu	Thr	Gly	Arg	Ile	Ser
			260					265					270		
His	Gly	Gln	Val	Asp	Leu	Ser	Glu	Leu	Gly	Pro	Asn	Ala	Asp	Glu	Leu
		275					280					285			
Leu	Ser	Lys	Val	Glu	His	Ile	Gln	Ile	Leu	Ala	Cys	Gly	Thr	Ser	Tyr
	290					295					300				
Asn	Ser	Gly	Met	Val	Ser	Arg	Tyr	Trp	Phe	Glu	Ser	Leu	Ala	Gly	Ile
305					310					315					320
Pro	Cys	Asp	Val	Glu	Ile	Ala	Ser	Glu	Phe	Arg	Tyr	Arg	Lys	Ser	Ala
				325					330					335	
Val	Arg	Arg	Asn	Ser	Leu	Met	Ile	Thr	Leu	Ser	Gln	Ser	Gly	Glu	Thr
			340					345					350		
Ala	Asp	Thr	Leu	Ala	Gly	Leu	Arg	Leu	Ser	Lys	Glu	Leu	Gly	Tyr	Leu
		355					360					365			
Gly	Ser	Leu	Ala	Ile	Cys	Asn	Val	Pro	Gly	Ser	Ser	Leu	Val	Arg	Glu
	370					375					380				
Ser	Asp	Leu	Ala	Leu	Met	Thr	Asn	Ala	Gly	Thr	Glu	Ile	Gly	Val	Ala
385					390					395					400
Ser	Thr	Lys	Ala	Phe	Thr	Thr	Gln	Leu	Thr	Val	Leu	Leu	Met	Leu	Val
			405						410					415	
Ala	Lys	Leu	Ser	Arg	Leu	Lys	Gly	Leu	Asp	Ala	Ser	Ile	Glu	His	Asp
			420					425					430		

GFAT-anglais

Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met Leu
435 440 445

Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp Lys
450 455 460

His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala Leu
465 470 475 480

Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Ala
485 490 495

Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Ala
500 505 510

Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu Lys
515 520 525

Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu Tyr
530 535 540

Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met His
545 550 555 560

Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe Tyr
565 570 575

Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys Gly
580 585 590

Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
595 600 605

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<212> DNA
<213> Artificial sequence

<220>
<223> Primer

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<220>
<223> Primer

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44

<210> 16

GFAT-anglais

<211> 43
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 16
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43

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<220>
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36

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 <212> PRT
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<220>
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<400> 18
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<210> 19
 <211> 6
 <212> PRT
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<220>
 <223> hexa-histidine tag

<400> 19
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